SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Lobb, Roy R.

    (ii) TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease

    (iii) NUMBER OF SEQUENCES: 4

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE:
        (B) STREET:
        (C) CITY:
        (D) STATE:
        (E) COUNTRY:
        (F) ZIP:

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME:
        (B) REGISTRATION NUMBER:
        (C) REFERENCE/DOCKET NUMBER: :

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 312-715-1000
        (B) TELEFAX: 312-715-1234

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 360 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

```
(ix) FEATURE:
     (A) NAME/KEY: misc_feature
     (B) LOCATION: 1
     (D) OTHER INFORMATION: /note="pBAG159 insert: HP1/2 heavy
         chain variable region; amino acid 1 is Glu (E) but Gln (Q)
         may be substituted"

(ix) FEATURE:
     (A) NAME/KEY: CDS
     (B) LOCATION: 1..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
```

```
GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA      48
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
 2           6               11              16

GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT      96
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
         21              26              31

ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA      144
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
         36              41              46

AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG      192
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
 51              56              61

GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG      240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
 66              71              76                      81

CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA      288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
             86              91              96

GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA      336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
         101             106             111

GGG ACC ACG GTC ACC GTC TCC TCA                                      360
Gly Thr Thr Val Thr Val Ser Ser
         116             121
```

```
(2) INFORMATION FOR SEQ ID NO:2:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 120 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
 2           6                 11                    16

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
         21                26                    31

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
     36                41                46

Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
     51                56                61

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
 66                71                76                    81

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
             86                91                96

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
         101                106               111

Gly Thr Thr Val Thr Val Ser Ser
     116                121
```

(2) INFORMATION FOR SEQ ID NO:3:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 318 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: cDNA

       (ix) FEATURE:
           (A) NAME/KEY: CDS
           (B) LOCATION: 1..318
           (D) OTHER INFORMATION: /product= "HP1/2 light chain
                variable region"

       (ix) FEATURE:
           (A) NAME/KEY: misc_feature
           (B) LOCATION: 1
           (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
                chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA        48
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
 1               5                  10                  15

GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT        96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
               20                  25                  30

GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA       144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
           35                  40                  45

TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC       192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
           50                  55                  60

AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT       240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
 65                  70                  75                  80

GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC       288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
               85                  90                  95

ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC                               318
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
               100                 105
```

(2) INFORMATION FOR SEQ ID NO:4:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 106 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
 1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
               20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
           35                  40                  45
```

Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65   70   75   80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
            85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
        100   105